

1 agggagaggc agtgaaccatg aaggctgtgc tgcctgccct gttgattgca  
51 ggcttggccc tgcagccagg cactgccctg ctgtgctact cctgcaaagc  
101 ccaggtgagc aacgaggact gccctgcaggt ggagaactgc acccagctgg  
151 gggagcagtg ctggaccgcg cgcatccgcg cagtggcct cctgaccgtc  
201 arcagcaaag gctgcagctt gaactgcgtg gatgactcac aggactacta  
251 cgtgggcaag aagaacatca cgtgctgtga caccgacttg tgcaacgcc  
301 gcgggggcca tgccctgcag ccggctgccg ccatccttgc gctgtccct  
351 gcactcggcc tgcctgtctg gggacccggc cagctatagg ctctgggggg  
401 ccccgctgca gccacactg ggtgtggtgc ccagggcctt tgtgccactc  
451 ctacagaac ctggcccagt gggagcctgt cctggttcct gaggcacatc  
501 ctaacgcaag ttgaccaatg tatgtttgca cccctttcc cnaaccctg  
551 acctcccat gggcctttc caggattccn accnnggcaga tcagtittag  
601 tganacanat ccgcttgcag atggccctc caaccntttt tgttgntgtt  
651 tccatggccc agcattttc acccttaacc ctgtgttcag gcacttttc  
701 cccaggaag cctccctgc ccaccccat tatgaattga gccaggttg  
751 gtccgtgggtg tccccgcac ccagcagggg acaggcaatc aggagggccc  
801 agtaagggt gagatgaagt ggactgagta gaactggagg acaagagttg  
851 acgtgagttc ctgggagttt ccagagatgg ggcctggagg cctggaggaa  
901 ggggccaggc ctacattg tggggtccc gaatggcagc ctgagcacag  
951 cgtaggccct taataaacac ctgtggata agccaaaaaa aaaaaaaa

MKAVLLALLMAGLALQPGTALLCYSCKAQVS NEDCLQV  
 ENCTQLGEQCWTARIRAVGLLTVISKGCSLNCVDDS  
 QDYYVGKKNITCCD TDL CNASGAHALQPAAAILALLPAL  
 GLLLWGPGQL

Figure 1B

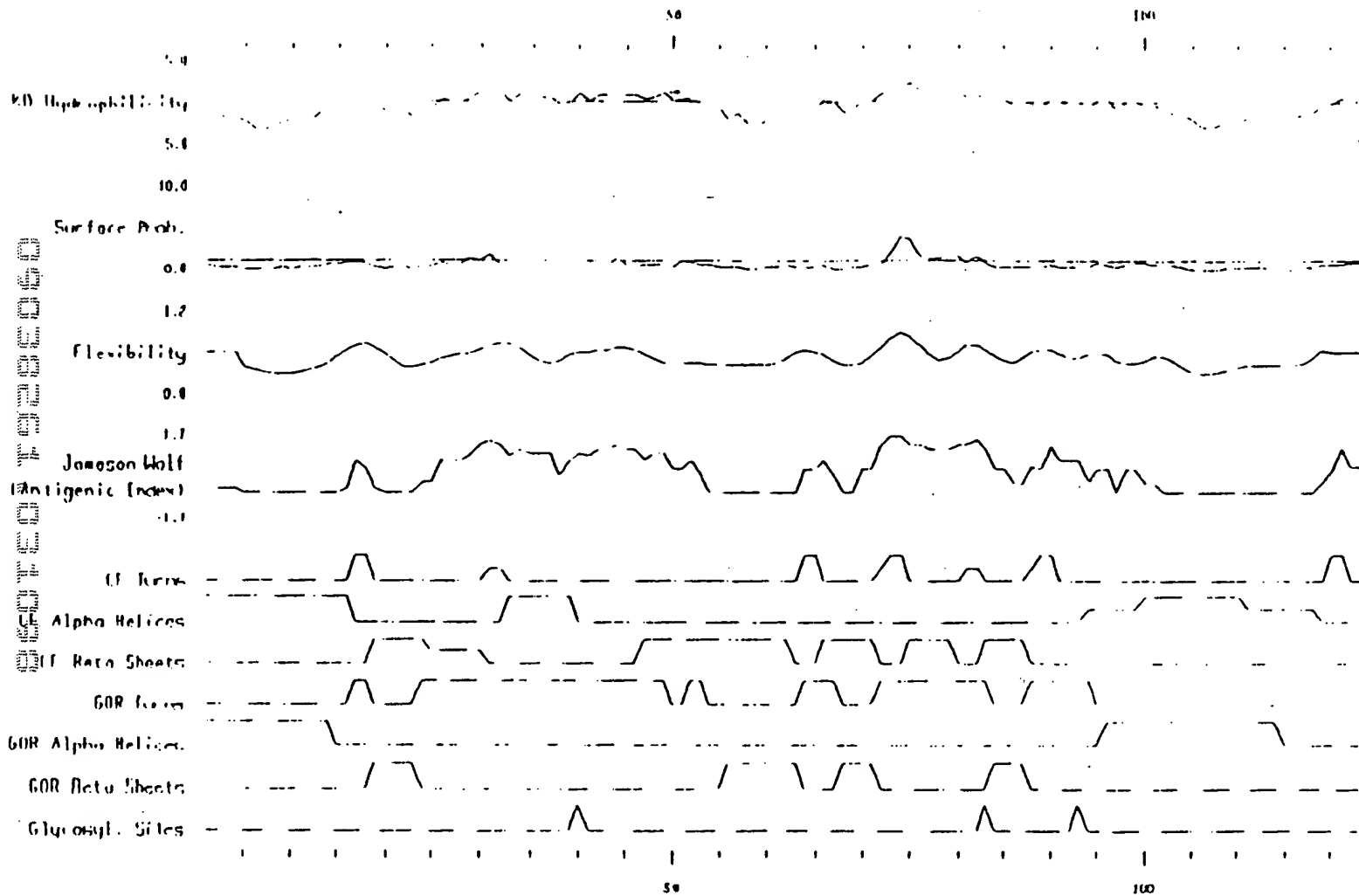
ATGAAGACAGTTTTTTTTATCCTGCTGGCCACCTACTTAGCCCTGCATCCAGGTGCTGCT  
1 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60  
TACTTCTGTCAAAAAAATAGGACGACCGGTGGATGAATCGGGACGTAGGTCCACGACGA  
M K T V F F I L L A T Y L A L H P G A A -  
CTGCAGTGCTATTTCATGCACAGCACAGATGAACAACAGAGACTGTCTGAATGTACAGAAC  
61 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 120  
GACGTCACGATAAGTACGTGTCGTCTACTTGTGTCTCTGACAGACTTACATGTCTTG  
L Q C Y S C T A Q M N N R D C L N V Q N -  
TGCAGCCTGGACCAGCACAGTTGCTTTACATCGCGCATCCGGGCCATTGGACTCGTGACA  
121 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 180  
ACGTCGGACCTGGTTCGTGTCAACGAAATGTAGCGCGTAGGCCCGGTAACCTGAGCACTGT  
C S L D Q H S C F T S R I R A I G L V T -  
GTTATCAGTAAGGGCTGCAGCTCACAGTGTGAGGATGACTCGGAGAACTACTATTGTTGGGC  
181 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 240  
CAATAGTCATTCCCGACGTGAGTGTCACTCCTACTGAGCCTCTTGATGATAAACCCG  
V I S K G C S S Q C E D D S E N Y Y L G -  
AAGAAGAACATCACGTGCTGCTACTCTGACCTGTGCAATGTCAACGGGGCCACACCCTG  
241 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 300  
TTCTTCTTGTAGTGACGACGATGAGACTGGACACGTTACAGTTGCCCCGGGTGTGGGAC  
K K N I T C C Y S D L C N V N G A H T L -  
AAGCCACCCACCCACCTGGGGCTGCTGACCGTGTCTGACGCTGTTGCTGTGGGGCTCC  
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 360  
TTCGGTGGGTGGTGGGACCCCGACGACTGGCACGAGACGTGGGACAACGACACCCCGAGG  
K P P T T L G L L T V L C S L L L W G S -  
AGCCGTCTGTAGGCTCTGGGAGAGCCTACCATAGCCCGATTGTGAAGGGATGAGCTGCAC  
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 420  
TCGGCAGACATCCGAGACCCTCTCGGATGGTATCGGGCTAACACTTCCCTACTCGACGTG  
S R L \*  
TCCACCCACCCACACAGG  
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 441  
AGGTGGGGTGGGGTGTGTCC

050700 192000Z

1 M K I F L P V L L A S L L G V E R A S S hSCA-2  
 1 M K A V L L L A L L M A G L A L O P G T A hPSCA  
 1 M K T V L L L L L A T Y L A L H P G A A mPSCA  
  
 21 L M C F S C L N Q K S N L Y C L K P T I  
 21 L L C Y S C K A Q V S N E D C L Q V E N  
 21 L Q C Y S C T A Q M N N R D C L N V Q N  
  
 41 C S D Q D N Y C V T V S A S A G I G N L  
 41 C T Q L G E Q C W T A R I R A V G L L T  
 41 C S L D Q H S C F T S R I R A I G L V T  
  
 61 V T F G H S L S K T C S P A C P I P E G  
 61 V - - - - I S K G C S L N C V D D S Q  
 61 V - - - - I S K G C S S Q C E D D S E  
  
 81 V N V G V A S M G I S C C Q S F L C N F  
 76 D Y Y V G K K - N I T C C D T D L C N A  
 76 N Y Y L G K K - N I T C C Y S D L C N V  
  
 101 S A A D G G L R A S V T L T G A G L L L  
 95 S G A H A L O P A A A I L A L L P A L G  
 95 N G A H T L K P P T T L G L L T V L C S  
  
 121 S L L P A L L R F G P  
 115 L L L W G P G O L - -  
 115 L L L W G S S R L - -

050302Z1034000

FIG. 4



signal  
sequence

□ = glycosylation site

✓ GPI signal

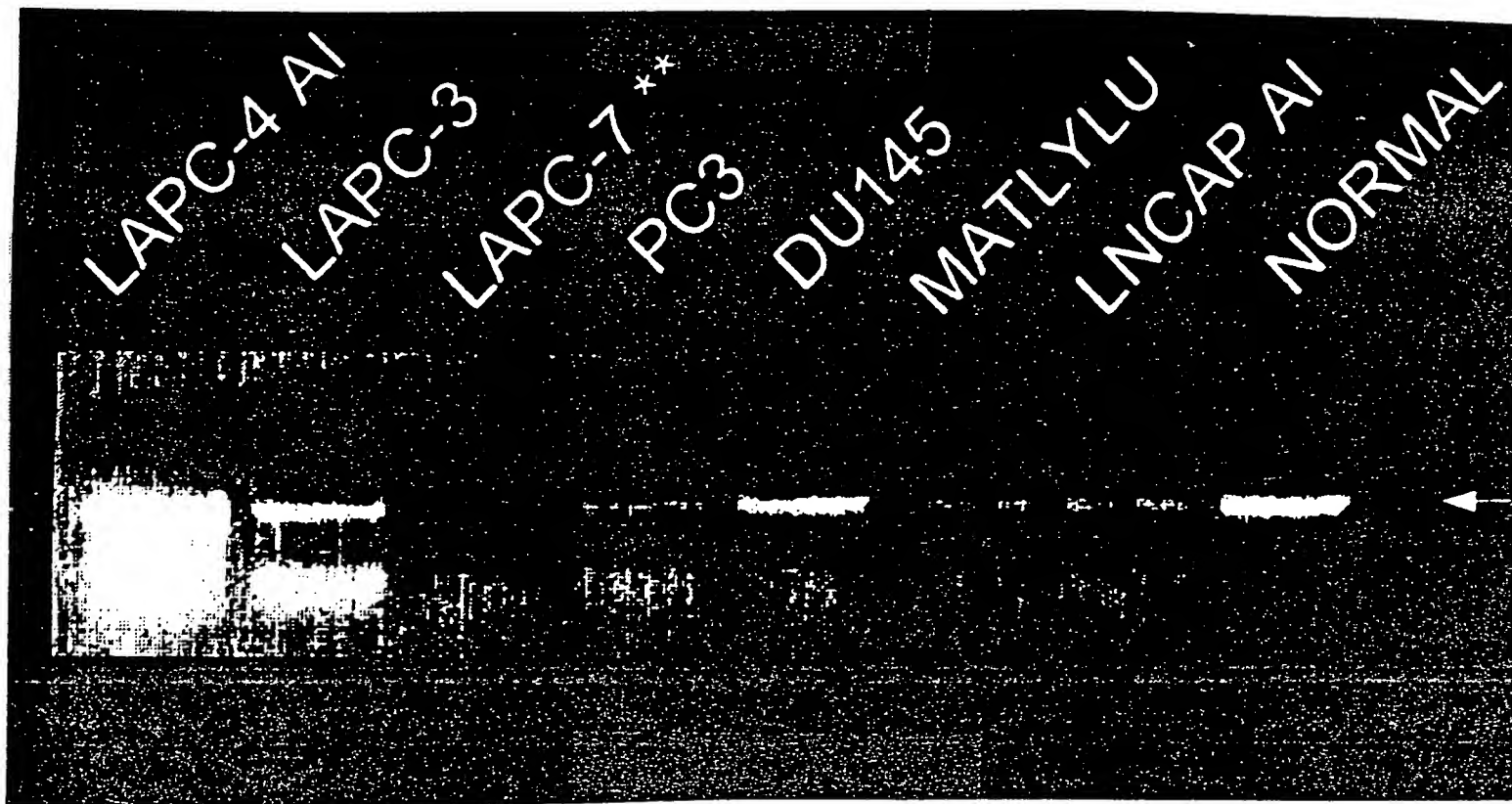
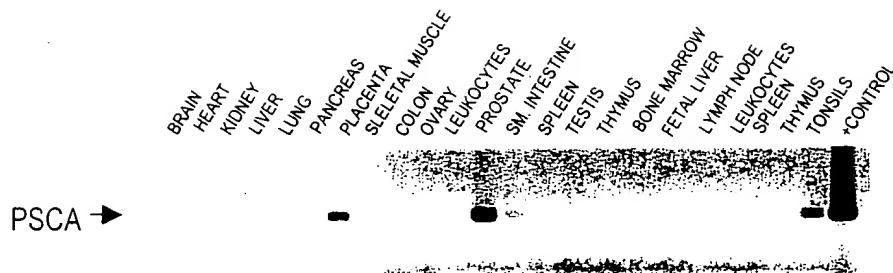
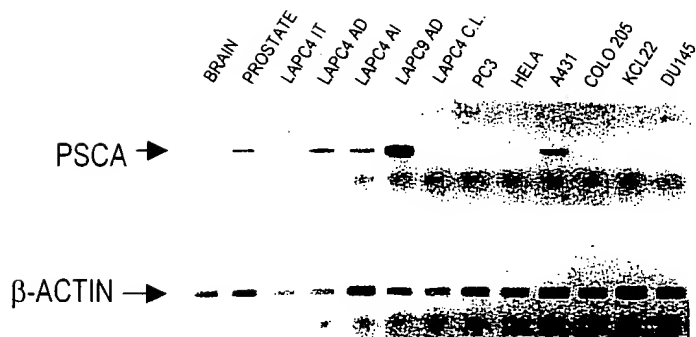


FIG. 7

A

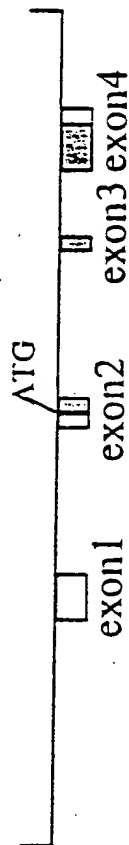


B

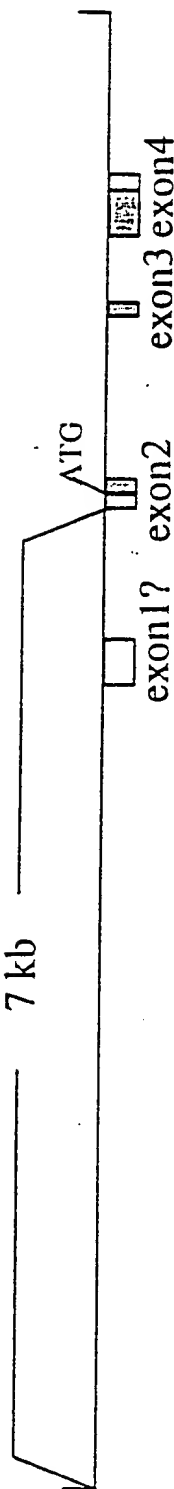




A. Ly-6/Thy-1 gene



B. mouse PSCA genomic clone (9 kb)



C. human PSCA genomic clone (14 kb)

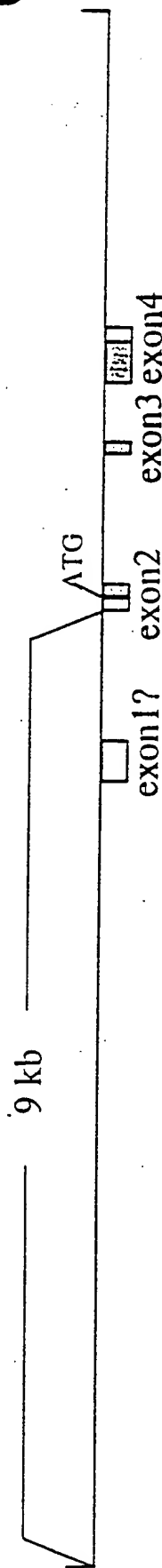


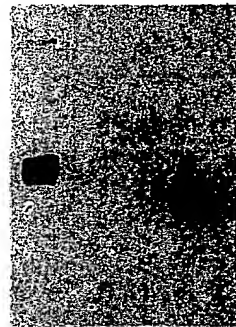
FIG. 15.

1G8

3E6

GST-PSCA  
GST-N-Terminal  
GST-Middle  
GST-C-Terminal

GST-PSCA  
GST-N-Terminal  
GST-Middle  
GST-C-Terminal



050302064.0340990

FIG. 14.

950760 1922060

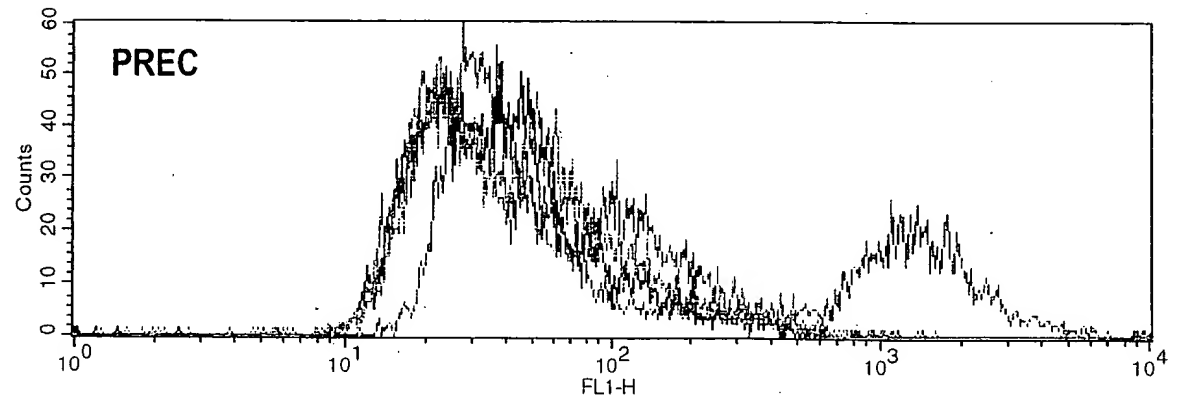
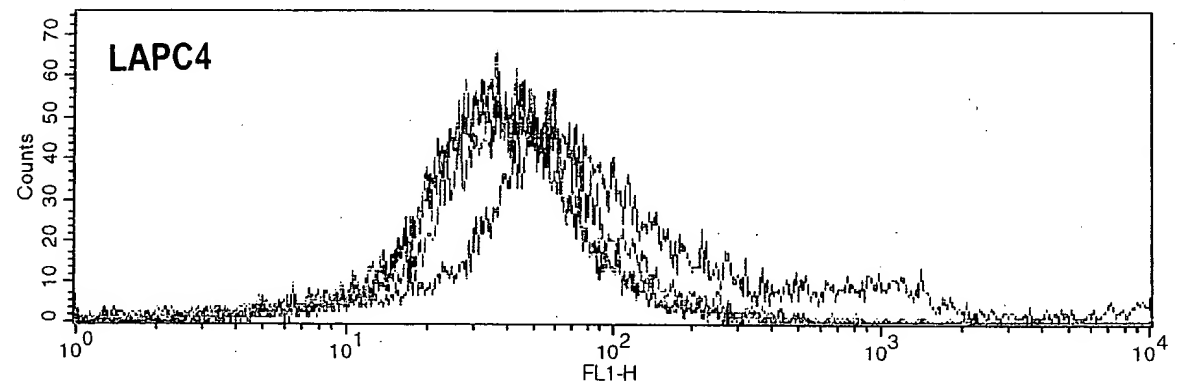
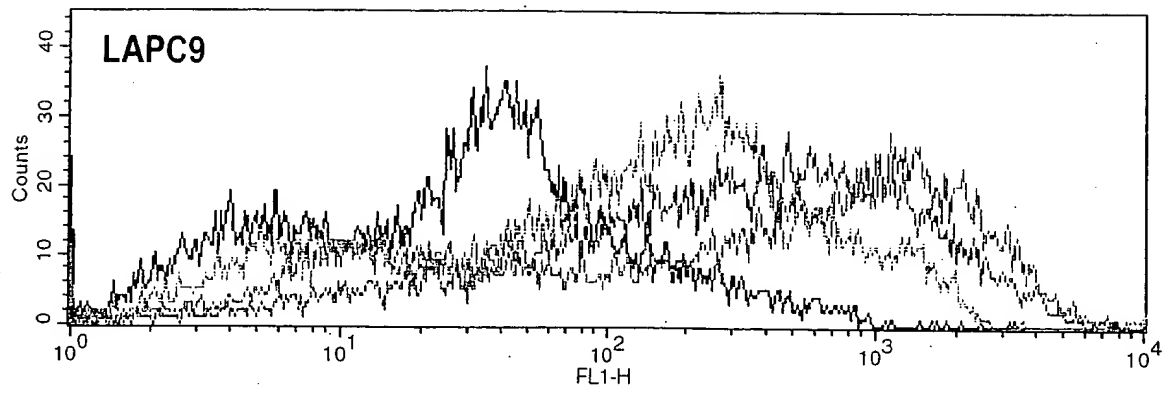
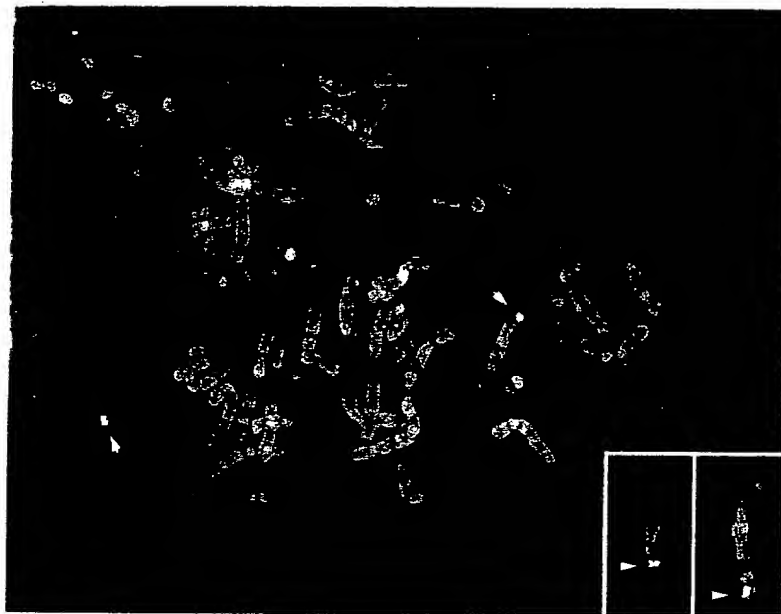


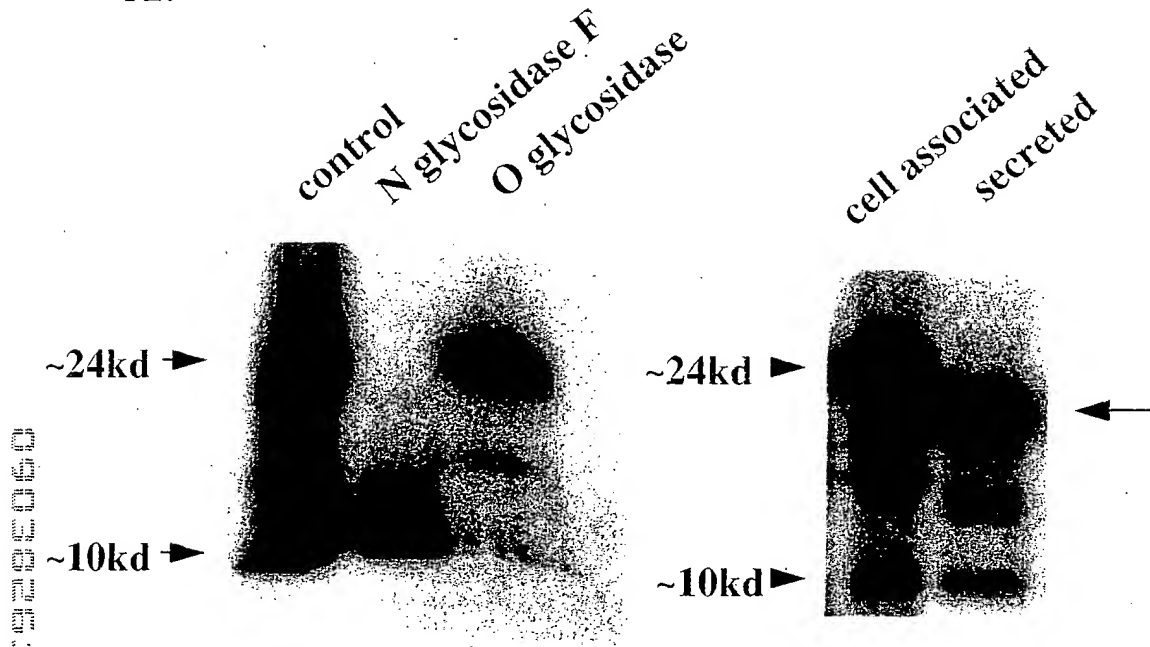
FIG. 13



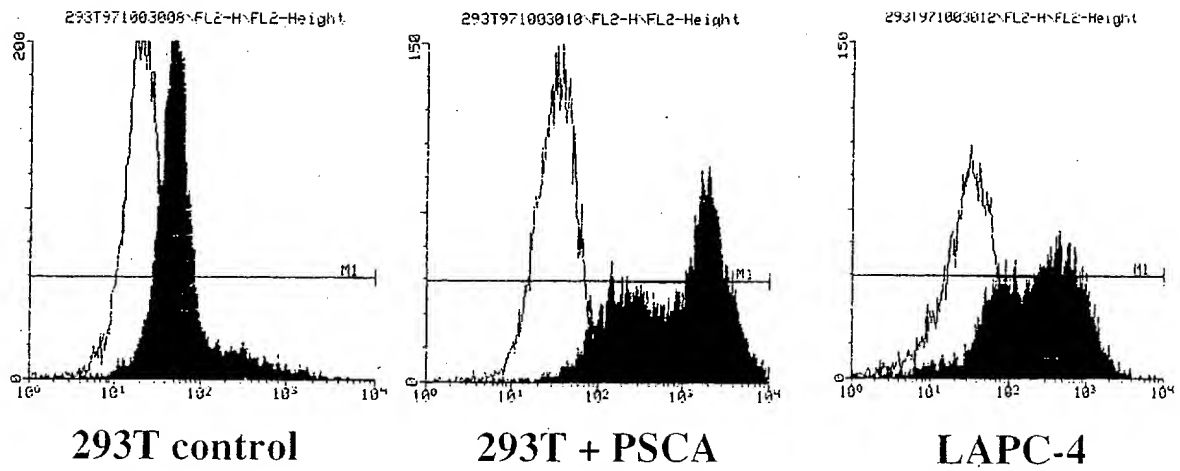
09038264.031098

A.

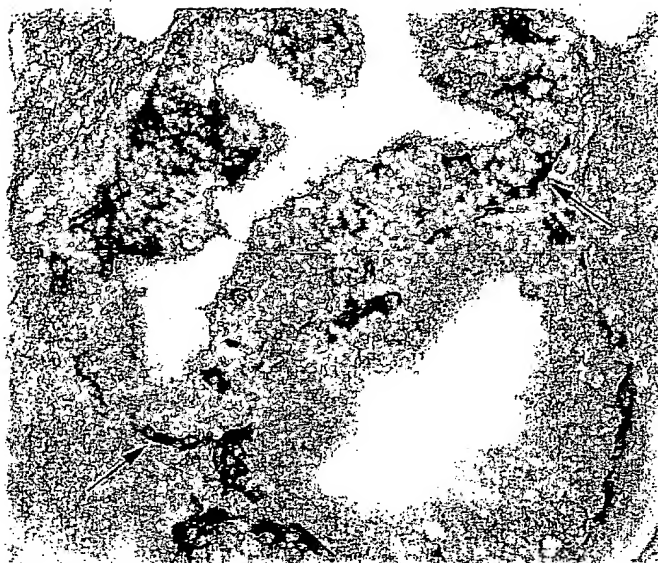
B.



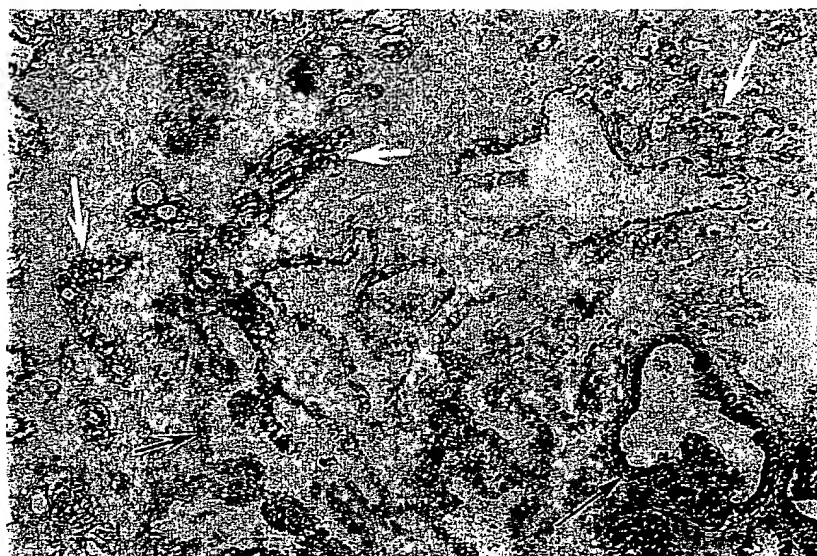
C.



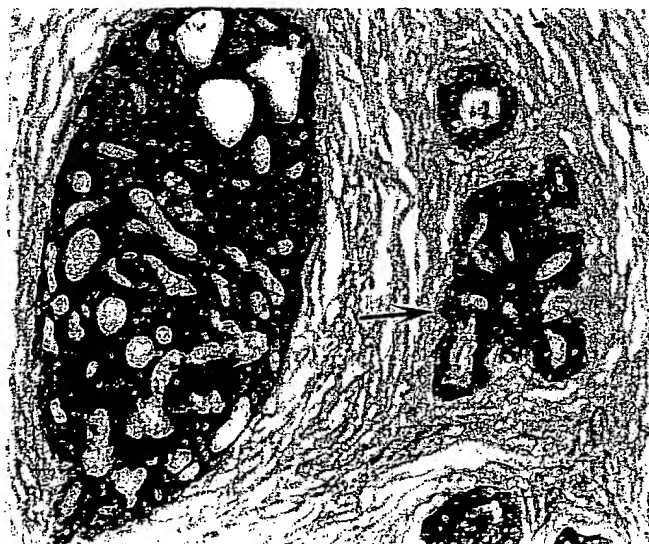
A.



B.



C.



09038261.031058

72 HRS

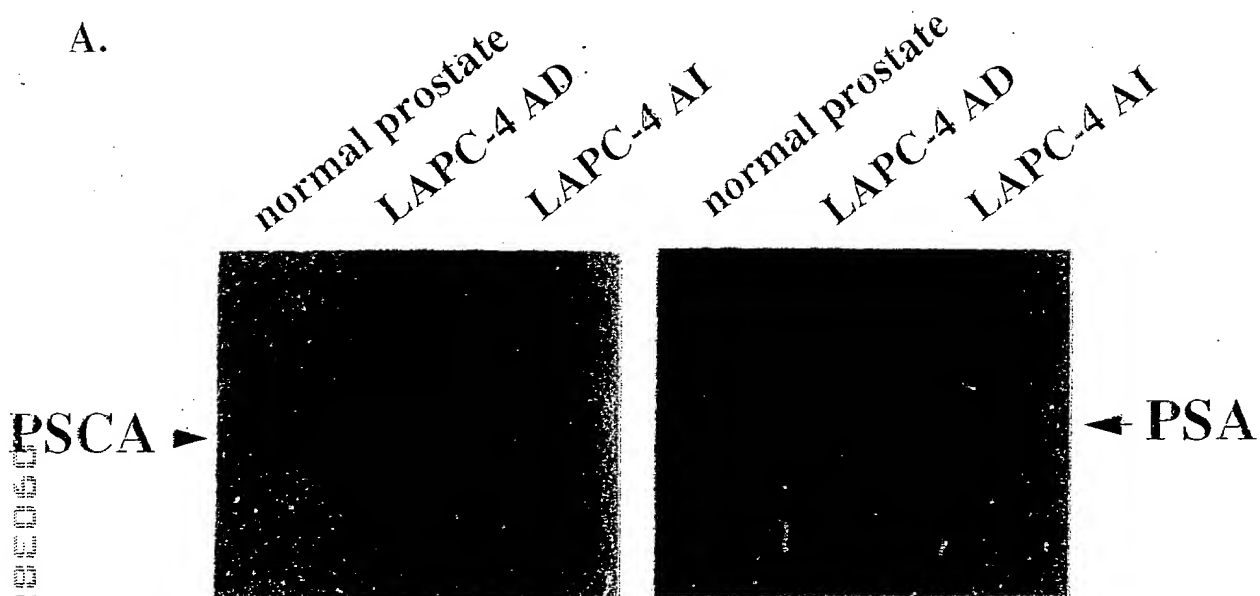
BPH  
LAPC4 AD  
LAPC4 AI  
LAPC4 IT  
LAPC9  
LAPC3 AI  
LAPC4 C.L.  
LNCAP  
PC3  
DU145  
HELA  
A431  
COLO 205  
KCL22

BPH  
LAPC4 AD  
LAPC4 AI  
LAPC4 IT  
LAPC9  
LAPC3 AI  
LAPC4 C.L.  
LNCAP  
PC3  
DU145  
HEL4  
A431  
COLO 205  
KCL22

BPH  
LAPC4 AD  
LAPC4 AI  
LAPC4 IT  
LAPC9  
LAPC3 AI  
LAPC4 C.L.  
LNCaP  
PC3  
DU145  
HELA  
A431  
COLO 205  
KCL22

FIG. 9

A.



B.

